

09896522-062801

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M A S A G G E D C E S P A P E A 16 SEQ ID NO:2

GAGCGGAGGCCGAG ATG GCT TCG GCG GGA GGC GAA GAC TGC GAG AGC CCC GCG CCG GAG GCC 43

↑SEQ ID NO:3→

D R P H Q R P F L I G V S G G T A S G K 36

GAC CGT CCG CAC CAG CGG CCC TTC CTG ATA GGG GTG AGC GGC GGC ACT GCC AGC GGG AAG 108

S T V C E K I M E L L G Q N E V E Q R Q 56

TCG ACC GTG TGT GAG AAG ATC ATG GAG TTG CTG GGA CAG AAC GAG GTG GAA CAG CGG CAG 168

R K V V I L S Q D R F Y K V L T A E Q K 76

CGG AAG GTG GTC ATC CTG AGC CAG GAC AGG TTC TAC AAG GTC CTG ACG GCA GAG CAG AAG 228

A K A L K G Q Y N F D H P D A F D N D L 96

GCC AAG GCC TTG AAA GGA CAG TAC AAT TTT GAC CAT CCA GAT GCC TTT GAT AAT GAT TTG 288

M H R T L K N I V E G K T V E V P T Y D 116

ATG CAC AGG ACT CTG AAG AAC ATC GTG GAG GGC AAA ACG GTG GAG GTG CCG ACC TAT GAT 348

F V T H S R L P E T T V V Y P A D V V L 136

TTT GTG ACA CAC TCA AGG TTA CCA GAG ACC ACG GTG GTC TAC CCT GCG GAC GTG GTT CTG 408

F E G I L V F Y S Q E I R D M F H L R L 156

TTT GAG GGC ATC TTG GTG TTC TAC AGC CAG GAG ATC CGG GAC ATG TTC CAC CTG CGC CTC 468

F V D T D S D V R L S R R V L R D V R R 176

TTC GTG GAC ACC GAC TCC GAC GTC AGG CTG TCT CGA AGA GTT CTC CGG GAC GTG CGC CGA 528

G R D L E Q I L T Q Y T T F V K P A F E 196

GGG AGG GAC CTG GAG CAG ATT CTG ACG CAG TAC ACC ACC TTC GTG AAG CCG GCC TTC GAG 588

E F C L P T K K Y A D V I I P R G V D N 216

GAG TTC TGC CTG CCG ACA AAG AAG TAT GCC GAT GTG ATC ATC CCA CGA GGA GTG GAC AAT 648

M V A I N L I V Q H I Q D I L N G D I C 236

ATG GTT GCC ATC AAC CTG ATC GTG CAG CAC ATC CAG GAC ATT CTG AAT GGT GAC ATC TGC 708

K W H R G G S N G R S Y K R T F S E P G 256

AAA TGG CAC CGA GGA GGG TCC AAT GGG CGG AGC TAC AAG CGG ACC TTT TCT GAG CCA GGG 768

D H P G M L T S G K R S H L E S S S R P 276

GAC CAC CCT GGG ATG CTG ACC TCT GGC AAA CGG TCA CAT TTG GAG TCC AGC AGC AGA CCC 828

H * 278

CAC TGA 834

←SEQ ID NO:3↑

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CACTGCTTCCTCTCGGCGCACCCCAGGGAGTGTTAGCAGCGAGGCCTTCCTCACTCAGGAGTGGAAGTCACTGATGTGT

CACTCAGACTCAACTTGCTGGGACTGACAGGCGTTCTGAGGTTTTCAGCCACTTAGGCTCGTTGCGGTTTAAAGAT

CCCTCTAGGTCACTGAGAAATGCCACAGAATGTGCAGGAAGCCTGGGAGGCTTCTGTGAGGAATGTGAGGCACATTATT

FIGURE 1a

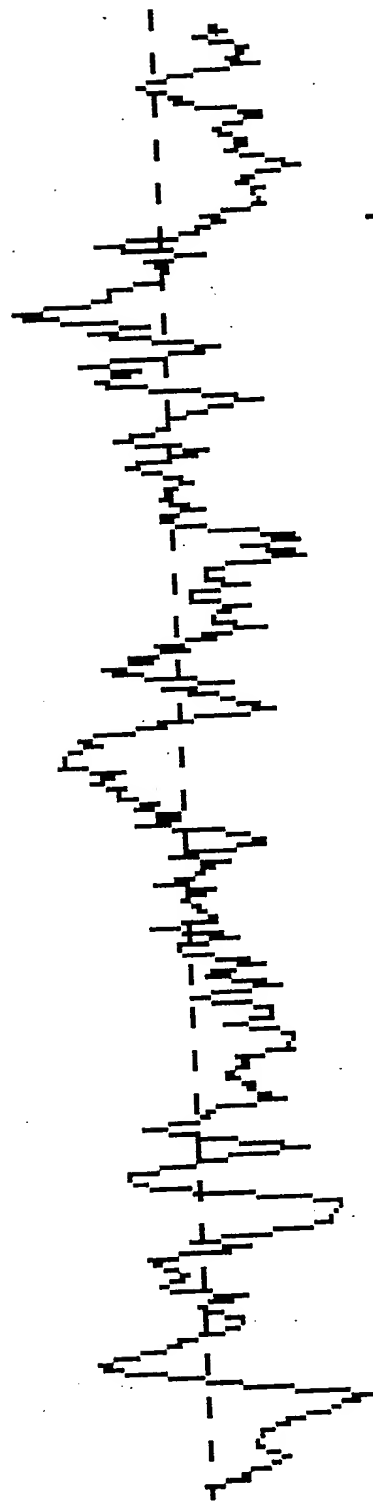
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GTGGTTTGCAGTCCAGCGTGGCCTACACGGATATGGGGAGCCACTGAGGGATGTTTTCCCCCCTTGCTTGTGCCTTAAA
GGCAGAGAAGCGAGGCGGATGCCCTGGAAGCACCCAGCATCACACCCAGGCTTGTGCGGGGCCAG

FIGURE 1b

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PFAH



C85

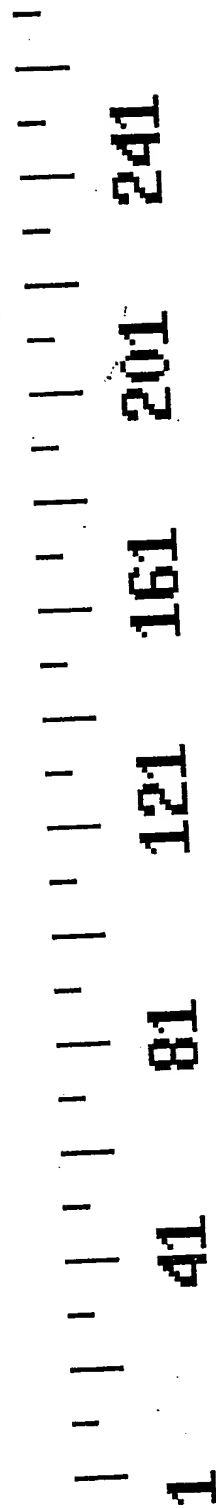


FIGURE 2

*->vIGvAGsSGaGKTTvarrivsifgregvpaagiEGnpDsNtgdsflr SEQ ID NO:4
 +IGv G+ ++GK+tv ++i ++g+ v +++l+
 25 LIGVSGGTASGKSTVCEKIMELLGQNEVE-----QRQRKVILS 63

 ldrfymdlhledrkragnkhysffsPeAndFDLLyevfkeLkeGksvdkP
 drfy++l++e+++ a + +y+f+ P A+d DL+ +++k+ eGk+v++P
 64 QDRFYKVLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP 113

 iYnHvtgerdpdggePGtFTdwpeliegadvLviEGLHalyDerevNvaq
 +Y++vt++r p ++ +++++adv+ +EG++ +y +++
 114 TYDFVTHSRLP-----ETTVVYPADVVLFEGLVVFYSQE---IRD 150

 LlDlkiyvDpdidlelarKiqRDmaeRGhsIEgvldsiekrrKPdyvNYI
 l ++vD+d+d++l+r+ RD+ RG++lE +l ++ +++KP+++ +
 151 MFHLRLFVDTDSDVRLSRRVLRDV-RRGRDLEQILTQYTTFFVKPAFEFEC 199

 aPQfsyaDliiqrvptvdtstndFiakiipvrdel<-*
 P+++yaD+ii+r+ ++ +++++ ++++++ d+l
 200 LPTKKYADVIIIPRGVDNMVAIN--LIVQHIQDIL 231

FIGURE 3

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Query: 154 LRLFVDTXXXXXXXXXXXXXXXXXXXXX-EQILTQYTTFVKPAFEEFCLPTKKYADVIIPR 212
 L++FVDT E ++ QY FVKP +E+F PTKKYAD+IIPR
 Sbjct: 1 LKIFVDTDADVRLIRRIKRDVNERGRDIESVIEQYMKFVKPMYEQFIEPTKKYADIIIPR 60 SEQ ID NO:5

Query: 213 GVDNMVAINLIVQHIQDILNGDICKWHRGGSNGRSYKRTFSEPGDHPGMLTSGKRSHLES 272
 G DN VAI+LIVQHIQ ILN + H RSYKRTFSEPGDHPG SGKR HLES
 Sbjct: 61 GGDNHVAIDLIVQHIQSILNEGLSSQHTNYMVNRSYKRTFSEPGDHPGYTPSGKRQHLES 120

Query: 273 SSRPH 277
 SSRPH
 Sbjct: 121 SSRPH 125

FIGURE 4

Query: 25 LIGVSGGTASGKSTVCEKIMELLGONEVEQRQRKVVILSQDRFYKVLTAEQKAKALKGQY 84
 +IG++GG+ SGK+T+ KI+E+L + Q KVVI+SQD +YK L+ + + Y
 Sbjct: 4 IIGIAGGSGSGKTTIARKIVEMLNK---PGQEKVVIISQDNYKDLSELDMEERKENNY 59 SEQ ID NO:6

Query: 85 NFDHPDAFDNDLMHRTLKNIVEGKTVEVPTYDFVTHSRLPETTV-VYPADVVLFEGLILVF 143
 NFDHPDAFD DL++ LK++ GK+VEVP YDF TH R + TV + PADV++ EGI
 Sbjct: 60 NFDHPDAFDLDLLYHLKBLKNGKSVEVPIYDFKTHHRRKDETVTIEPADVILEGIYAL 119

Query: 144 YSQEIRDM 151
 Y + IRD+
 Sbjct: 120 YDERIRDL 127

FIGURE 5

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